

**SUPERIOR COURT OF THE DISTRICT OF COLUMBIA
Criminal Division – Felony Branch**

UNITED STATES OF AMERICA	:	
	:	Criminal No. F-320-00
v.	:	Judge: Broderick
	:	Trial: April 19, 2004
	:	
RAYMOND JENKINS	:	

**MOTION TO EXCLUDE DNA “INCLUSION” EVIDENCE, EXPERT TESTIMONY, AND
FREQUENCY STATISTICS BECAUSE THERE IS NO GENERAL ACCEPTANCE AS TO
THE STATISTICAL METHODS OF INTERPRETATION OF DNA EVIDENCE THAT
DERIVES FROM A “COLD HIT” IN A DNA DATABASE, WITH POINTS AND
AUTHORITIES IN SUPPORT**

Raymond Jenkins, through undersigned counsel, respectfully moves this Honorable Court, pursuant to *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923), *Dyas v. United States*, 376 A.2d 827 (D.C. 1977), *United States v. Porter*, 618 A.2d 629 (D.C. 1990) (“*Porter II*”),¹ *Daubert v. Merrell Dow Pharm.*, 509 US. 579 (1993), and the Due Process Clause of the Fifth Amendment, to exclude all DNA evidence and testimony from the government’s case. Mr. Jenkins notes that, as the proponent of the scientific evidence, the government bears the burden to prove its evidence is admissible and submits that the government cannot carry its burden. The statistics proffered by the government to explain the significance of the alleged “inclusion” are currently the subject of a raging debate with scientists divided into three separate camps calling for three starkly different approaches. *See* Section II, *infra*. The Court of Appeals has made clear that the presentation of a statistical calculation is *required* to admit DNA evidence. This Court should preclude the government’s introduction of DNA evidence in this case until the debate is quelled and a generally

¹ Mr. Jenkins refers to Judge Kennedy’s underlying trial decision, *United States v. Porter*, Crim. No. F-6277-89, 1991 WL 319015 (D.C. Super. Sept. 20, 1991) as “*Porter I*” and the Court of Appeals decision in the case, cited above, as “*Porter II*.”

accepted approach is developed. Mr. Jenkins requests a hearing on this Motion.²

Overview

The DNA evidence in this case derives from a novel technique that has not been admitted in any case in the District of Columbia. According to the government, Mr. Jenkins became a suspect upon the “cold hit” of a DNA STR profile purporting to be his in a large databank maintained by Virginia. The statistical significance of such a databank, or “cold hit” is a matter of continuing and strident debate. Because no statistical method is generally accepted for expressing the significance of a “cold hit,” the government’s efforts to introduce any DNA evidence in this case must fail.

Until recently, the DNA STR profiles that have been generated for forensic purposes in this jurisdiction (and, for that matter, nationwide) have exclusively been those that could be characterized as “confirmation matches,” in which DNA STR testing has been performed upon a reference sample taken from a suspect who has already been linked to a crime by direct or circumstantial evidence. Mr. Jenkins’ case presents Superior Court’s first example of a new type of DNA STR profile “match” – one that was generated as a result of a “cold hit” from the trawling of a large number of DNA profiles maintained in a convicted offender database. As the primary difference between these kinds of matches is the manner in which a suspect is first identified, it is impossible to convert one type of case into the other (for instance, by simply retesting a reference sample once a “cold hit” has been identified). Instead, the statistical significance of these two kinds of DNA profile matches must be determined differently. On this point, there is broad scientific consensus.

However, the necessary next step of determining the statistical value of the “cold hit” is buried in scientific controversy: There are at least three different commonly held, and strikingly

² The defense notes that discovery requests with the government are ongoing and reserves the right to supplement this Motion upon the receipt of additional discovery.

different and conflicting opinions as to how the statistics associated with DNA profiles generated after a “cold hit” should be calculated and presented. In short, there is no general acceptance of the scientific significance of the purported “cold hit” proposed by the government.

As noted, this case constitutes the first time that the government has prosecuted a “cold hit” DNA case in which a suspect is identified by the trawling of a crime scene DNA profile through a convicted offender database. In addressing the admissibility of DNA evidence in the joint litigation of *United States v. Orlando Roberts*, F-771-01, and *United States v. David Veney*, F-3986-00 [“*Roberts/Veney*”],³ the Honorable Robert I. Richter opined that, as opposed to those cases where the DNA simply corroborated a complainant’s report that she had been sexually assaulted by a named defendant, a challenge to the admissibility of DNA evidence deserved special, heightened scrutiny in “cold hit” cases where the science itself is the lodestar of the government’s evidence against the defendant.

Mr. Jenkins wishes to make clear that the issues presented in this Motion are unique to “cold hit” cases and therefore were not presented before Judge Richter. Rather, this Motion – challenging the admissibility of DNA STR evidence in a “cold hit” case -- presents an issue of first impression in this jurisdiction. Indeed, because the development of convicted offender DNA databases and the trawling of such databases to identify suspects is a recent phenomenon, there are no published opinions from any jurisdiction that address the admissibility of such evidence at trial. In a separate pleading filed last week, Mr. Jenkins raised the issues litigated in the *Roberts/Veney* litigation and encouraged this Court to consider those issues *ab initio*. While a grant of that motion would result in either the exclusion of the evidence or the requirement that the government carry its burden at an

³ Judge Richter declined to hold a *Frye* hearing in that litigation, instead asking for written pleadings and affidavits from the parties and ultimately denying the motions to exclude on the papers after a colloquy with the parties addressing the issues.

evidentiary hearing, a denial of that motion has no consequence on the issues raised here.

Mr. Jenkins also wishes to make clear that, as the proponent of the evidence, the government bears the burden to establish that there is a general consensus in the scientific community over how DNA STR matches derived from “cold hits” should be analyzed and presented, and that the government cannot meet its burden in light of the controversy in the relevant scientific community. Mr. Jenkins is not arguing – for he is not required to – that one approach or another is preferred: The existence of controversy, the lack of consensus alone requires exclusion under *Frye*.

In addition to his *Frye/Dyas* claim, Mr. Jenkins also moves to exclude the DNA evidence on evidentiary grounds. First, in light of the talismanic power of DNA evidence before juries, the admission of the DNA evidence is substantially more prejudicial than it is probative. Additionally, the government will be unable to prove chain of custody concerning the DNA sample alleged to be Mr. Jenkins that was placed in the convicted offender database and then used for comparison purposes. Thus, under both *Frye/Dyas* and the rules of evidence, this Court must exclude the government’s proffered DNA evidence.

I. ANALYTICAL FRAMEWORK

A. The *Frye/Dyas* Framework for Admissibility of Scientific Evidence in D.C.

The D.C. Court of Appeals has set forth three requirements for the admission of expert testimony on a given subject:

(1) [T]he subject matter must be so distinctively related to some science, profession, business, or occupation as to be beyond the ken of the average layman; (2) the witness must have sufficient skill, knowledge, or experience in that field . . . as to . . . aid the trier in his search for truth; and (3) expert testimony is inadmissible if the state of the pertinent art or scientific knowledge does not permit a reasonable opinion to be asserted even by an expert.

Dyas v. United States, 376 A.2d 827, 832 (D.C. 1977) (citations omitted). This test requires trial courts to find both that the technique relied upon by the expert has gained “general acceptance” in the scientific community, *Ibn-Tamas v. United States*, 407 A.2d 626, 638 n.23 (D.C. 1979) (third prong of *Dyas* requires “general acceptance”), and that the facts or data relied upon by the expert in rendering his or her opinion are sufficiently reliable to be “reasonably relied upon” by the expert. *United States v. Melton*, 597 A.2d 892, 901, 903 (D.C. 1991).

The “general acceptance” requirement of *Dyas* is equivalent to the well-known test of *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923), for admission of novel scientific evidence. *Dyas* and *Frye* require the proponent of the evidence to demonstrate by a preponderance of the evidence that the technology has been generally accepted in the relevant scientific community:

Just when a scientific principle or discovery crosses the line between the experimental and demonstrable stages is difficult to define. Somewhere in this twilight zone the evidential force of the principle must be recognized, and while courts will go a long way in admitting expert testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs.

Frye, 293 F. at 1014. *See also Yisrael v. State*, 827 So. 2d 1113, 1114 (Fla. Dist. Ct. App. 2002) (proponent has burden to show by preponderance of evidence that scientific method is generally accepted). When determining whether scientific evidence is “generally accepted,” trial judges do not play the role of scientist and independently determine the validity of a particular science or technique; rather, “[t]he issue is consensus versus controversy over a particular technique, not its validity. . . . If scientists significant either in number or expertise publicly oppose [a new technique] as unreliable, then that technique does not pass muster under *Frye*.” *Nixon v. United States*, 728 A.2d 582, 588 (D.C. 1999) (emphasis added). A court “may consider not only expert evidence of record, but also judicial opinions in other jurisdictions, as well as pertinent legal and scientific

commentaries.” *Porter II*, 618 A.2d at 635 (citing *Jones v. United States*, 548 A.2d 35, 41 (D.C. 1988)). By requiring that the scientific community approve of a technique, the *Frye/Dyas* test recognizes the limitations on courts’ ability to act as arbiters of scientific disputes: “[T]he court may not resolve a scientific dispute between opponents and proponents of the technique, [and] the very existence of the dispute precludes admission of the testimony.” *Porter*, 618 A.2d at 634 (citation omitted) (alteration in original). “A courtroom is not a research laboratory.” *Id.*

Thus, while the federal courts have shifted from *Frye* to a more lenient test based on Federal Rule of Evidence 702 that emphasizes “reliability” based upon “scientific validity” and rejects “general acceptance” as a mandatory requirement, *Daubert*, 509 U.S. at 590 n.9, D.C. has remained true to the “rigid” and “austere” general acceptance standard. *Id.* at 588, 589. On the other hand, because *Dyas* requires that scientific evidence in D.C. be both generally accepted *and* sufficiently reliable to be reasonably relied upon by the testifying expert, trial courts in D.C. maintain a “gate-keeping function” notwithstanding D.C.’s adherence to the *Frye* standard.

Safeguarding the courtroom from applications of scientific theories that are not generally accepted is especially crucial when dealing with evidence such as DNA, which has an aura of infallibility from its coverage in the popular press and from its almost mysterious quality. In rejecting expert testimony about lie detector tests, which equally capture the imagination of jurors, the D.C. Court of Appeals noted that “[b]ecause of the authoritative quality which surrounds expert opinion, courts must reject testimony which might be given undue deference by jurors and which could thereby usurp the truthseeking function of the jury.” *Proctor v. United States*, 728 A.2d 1246, 1249 (D.C. 1999) (quoting *Smith v. United States*, 389 A.2d 1356, 1359 (D.C. 1978)).

Thus, the government in this case must prove at a *Frye* hearing both that the interpretation and reporting methods used in its “cold hit” DNA analysis are generally accepted in the scientific

community. As discussed below, because of the raging controversy about the significance of a DNA “cold hit” and its effect on any subsequent comparisons and the lack of reliable information concerning the process that led to the “cold hit” in this case, the government cannot successfully show either general acceptance or reliability sufficient to pass muster under *Frye/Dyas*.

B. Forensic DNA Evidence is Inadmissible Without Accompanying Probability Statistics to Explain the Statistical Significance of a Match to Provide to the Jury.

As Judge Kennedy explained, the accuracy of the statistical expression of the significance of a reported “match” is “at the very core of DNA evidence” and goes to admissibility of the DNA evidence, not merely weight:

It is the proclaimed ability to tell a jury that the odds of a coincidental match is one in thirty million, more than twice the number of African American men in the United States, which makes it so potentially compelling. No matter what qualifiers precede the statistical expression one in thirty million, this is tantamount to saying that *Porter* was the donor of the questioned specimen, that he, in effect, left his fingerprint.

United States v. Porter, No. F-6272-89, 1991 WL 319015 at *26 (D.C. Sup. Ct. Sept. 20, 1991).

Judge Kennedy further explained that complex statistical issues should be resolved before trial as admissibility issues rather than through cross-examination or competing experts, because juries will naturally gravitate toward numbers and the “bottom line”:

It is almost certain that jurors would simply “jump” to the bottom line numbers without giving any meaningful consideration to any dispute over the principles, which underlie the methodology used to generate those numbers. To permit the fancy of jurors to operate in this manner is the antithesis of “due process.”

Id. at *27. The D.C. Court of Appeals agreed with Judge Kennedy, noting that such probability issues are subject to a *Frye* challenge:

“Since a match between two DNA samples means little without data on probability, the calculation of statistical probability is an integral part of the process and the underlying method of arriving at that calculation must pass muster under *Kelly/Frye*.” Axel, *supra*, 235 Cal. App. 3d at 866-67. “W[e] would not permit the

admission of test results showing a DNA match (a positive result) without telling the jury anything about the likelihood of that match occurring.” *Curnin, supra*, 409 Mass. at 222 n.7. Since the probability of a coincidental match is an essential part of the DNA evidence, and since there is no consensus as to the accuracy of the FBI’s calculation, we decline to hold that the defense objections to *that precise calculation* go only to its weight.

Porter II, 618 A.2d at 640. Thus, the government’s “underlying method of arriving at th[e] calculation” of the “likelihood of th[e] match occurring” is a proper focus of a *Frye* inquiry.

C. History of Virginia Convicted Offender Database, Raymond Jenkins’ Inclusion, and Report of “Cold Hit” in this Case.

The “cold hit” in this case arose from a search of the Virginia convicted offender DNA database. In 1989-90, Virginia established a DNA database and procedures for the Virginia Division of Forensic Sciences’ (“VDFS”) collection, analysis, and exchange of DNA information for the purpose of criminal law enforcement, *see* Va. Code Ann. §§ 19.2-310.02 through 19.2-310.7 (Michie 1990), and today, Virginia’s database is without question the largest such database in the nation. The legislation was initially passed in 1989 covering only felony sex offenders but was expanded in 1990 to all include all convicted offenders. The legislation was again expanded in 1996 to include all juveniles fourteen years and older who were convicted of what would be considered a felony of they had been charged as an adult.⁴

The VDFS’ analysis of convicted offender blood samples using DNA, under a procedure known by the acronym of RFLP, began in 1992. However, in mid-1997, the VDFS discontinued the use of the RFLP technique in the analysis of convicted offender samples in favor of STR/PCR

⁴ *See* George C. Li & Linda Johnston, *Observations Associated With CODIS Hits Obtained By Searching a Large DNA Databank* at 1, located at <http://www.promega.com/geneticidproc/ussymp11proc/content/li.pdf>.

technology. *Id.*⁵ Virginia continued to collect its convicted offender samples by drawing blood and analyzing the blood for the offender's STR profile. STR/PCR technology is now the dominant DNA typing technology.

At some point in the 1990s, Raymond Jenkins was convicted of an offense in Virginia. Prior to his release from incarceration, his DNA sample was allegedly seized from him for inclusion in Virginia's rapidly expanding convicted offender database. At that time, Virginia maintained convicted offender profiles at only 8⁶ different genetic locations (known as loci).⁷ The number of loci searched in the database is an essential factor considered by the different camps of battling statisticians. Notably, very shortly after the database "cold hit" in this case, the VDFS modified its procedure to obtain 13-loci DNA profiles of convicted offenders for its database;⁸ The VDFS now obtains 14-loci profiles for its database;⁹ and the VDFS' Director has stated that, at minimum, searchable databases should rely on 13-loci profiles.¹⁰

On November 16, 1999, Assistant U.S. Attorney Terence J. Keeney wrote the VDFS and asked it to compare the STR profiles in its DNA convicted offender database with an STR profile

⁵ The differences between the two technologies are great and are discussed in detail in *Porter I* and Defendant's Supplemental Motion to Exclude Nuclear DNA "Match" Evidence, DNA Expert Testimony, and "Random Match Probability" Calculation (April 2, 2004), at 11-14.

⁶ There are, of course, millions and millions, of different loci on the human genome.

⁷ The 8 profiled loci, determined by the Promega PowerPlex® 1.1 system, were CSF1PO, TPOX, TH01, vWA, D16S539, D7S820, D13S317, and D5S818. See Li & Johnston, *supra*, at 1; <http://www.promega.com/tbs/Tmd008/tmd008.pdf> (PowerPlex® 1.1 System Technical Manual No. D008) (listing PowerPlex® 1.1 loci).

⁸ See Li & Johnston, *supra*, at 1-2.

⁹ See VA DCJS – Laboratory Sections and Forensic Services – Frequently Asked Questions, located at <http://www.dcjs.org/forensic/sections/forensicBiology/faq.cfm> ("The Virginia Division of Forensic Science currently is using the Promega GenePrint™ 1.1 and 2.1 Systems, which include the SCFPO, TPOX, TH01, vWA, D16S539, D7S820, D13S317, D5S818, Penta E, D18S51, D21S11, D3S1358, FGA, and D8S1179 loci.").

¹⁰ See Paul B. Ferrara, Ph.D., Director, Virginia Division of Forensic Science, *Analysis of the First 1000 Database Hits and Implementation of Point of Arrest DNA Collection*, presented at 14th Int'l Symposium on Human Identification (Sept. 30, 2003).

from six crime scene samples of evidence (Q2-18, Q3-13, Q5-1, Q-11, Q-15, and Q-37) in this case. *See* Letter from Terence J. Keeney, Assistant U.S. Attorney, to Lisa Schiermeier, Forensic Science Supervisor (Nov. 16, 1999). The VDFS complied with the request and identified a “cold hit” DNA profile in its database that was “consistent with” the profile generated from the crime scene evidence. *See* Letter from Lisa C. Schiermeier, Forensic Scientist Supervisor, to Terence J. Keeney, Chief, Homicide Section, at 1 (Nov. 22, 1999).¹¹ Because of the risk of a coincidental match, Ms. Schiermeier qualified the significance of the “cold hit”: “This information is provided only as an investigative lead, and any possible connection or involvement of this individual to the case must be determined through further investigation.” *Id.* The government is proceeding on the theory that the Virginia profile is that of Mr. Jenkins.¹²

With the 8-loci “cold hit,” the government’s investigation of alternative suspects ceased. Testimony of Detective Garvey at February 25, 2000 Preventive Detention Hearing, at 57-58. The government then sought and obtained a search warrant for Mr. Jenkins’ blood and delivered his blood sample to the Federal Bureau of Investigation (“FBI”). The FBI analyzed Mr. Jenkins’ blood for his DNA types across 13 different loci – the same 8 loci that Virginia used to generate the profile in its database and an additional 5 loci¹³ -- and determined that the probability of finding Mr. Jenkins’ 13-loci DNA profile at random in the African-American population (also known as the random match probability or RMP) is 1 in 10,750,000,000,000,000, and that based upon that result of this 13-loci comparison, the FBI concluded that Mr. Jenkins is the sole contributor to the

¹¹ At that time, the Virginia database had between 100,000 and 125,000 profiles. *See* Li & Johnson, *supra* at 1,2.

¹² Ms. Schiermeier stated that “[t]he consistent profile was that of Robert P. Garrett, SSN #080-52-7396, DOB 02/25/61.” The Metropolitan Police Department searched NCIC records and concluded that Robert Garrett is also known as Raymond Jenkins, SSN #080-52-6161, DOB 02/25/61. Mr. Jenkins’ does not concede the NCIC search’s accuracy.

¹³ The additional five loci are D3S1358, FGA, D821179, D21S11, and D18S51

evidentiary blood samples to a reasonable degree of scientific certainty. The government has indicated that it will seek to admit this testimony at Mr. Jenkins' trial.

Virginia, of course, does not maintain the only convicted offender database in the country. At present, all fifty states and the federal government have convicted offender databases, and, with the exception of Mississippi, all are linked electronically. The FBI Laboratory's Combined DNA Index System (CODIS) enables federal, state, and local crime labs to exchange and compare DNA profiles electronically. CODIS began as a pilot program in 1990 serving fourteen state and local laboratories. The DNA Identification Act of 1994 formalized the FBI's authority to establish a national DNA index for law enforcement purposes. CODIS is a distributed database with three hierarchical levels (or tiers) – local, state, and national. The FBI's National DNA Index System (NDIS) is the highest level in the CODIS hierarchy and allows CODIS laboratories to exchange and compare DNA on a national level. All DNA profiles originate at the local level (LDIS) then flow to the state (SDIS) and national (NDIS) levels.

As the administer of the program, the FBI has taken steps to ensure uniformity among the jurisdictions in how they administer their individual database programs. Among the FBI's prescriptions was the setting of a core group of 13 genetic loci (known as the CODIS loci) that should always be tested regardless of the jurisdiction. Those are the same 13 loci that Virginia's crime lab director advocates all systems use and that Virginia began using *immediately after* the "cold hit" in this case, and that the FBI used for its comparison purposes in this case. Notably, no CODIS "hit" was returned in this case.

II. THE DNA EVIDENCE DOES NOT MEET THE *FRYE/DYAS* TEST BECAUSE THE INTERPRETION OF SUCH EVIDENCE, WHEN DERIVED FROM A "COLD HIT" OF A DNA DATABASE TRAWL, IS MIRED IN CONTROVERSY.

Because the "cold hit" derived from a trawl of Virginia's database, the proper statistical interpretation of its results are critical. The relevant scientific community of statisticians, mathematicians,

and population geneticists is divided as to the proper statistical approach to take in database search cases and as to the statistical effect on the random match probability number offered at trial when the defendant was initially identified through a DNA database cold hit. In simplest terms, some statisticians believe that the random match probability statistic *overestimates* the probability of inclusion when identification follows a cold hit and divide into two separate camps as to how to correct the overestimation, while others believe the exact opposite, that the random match probability statistic *underestimates* the probability of inclusion in such circumstances. No scientist agrees with the government's proposal to simply place before the jury the random match probability as one does in more traditional DNA "confirmation" cases like *Orlando Roberts*. Rather, the scientific community generally agrees that a "cold hit" case must always be treated differently statistically because "cold hit" cases are fundamentally different than "confirmation" cases. Because of the controversy over how significant DNA evidence is in a "cold hit" case, the government cannot carry its burden under *Frye/Dyas*, and this Court must exclude all DNA evidence at trial.

A. The Scientific Community Generally Agrees that a "Cold Hit" Cases Must Always Be Treated Differently in Explaining the Significance of the DNA Evidence Because "Cold Hit" Cases Are Fundamentally Different than "Confirmation" Cases.

A "cold hit" case must be treated differently than a "confirmation" case. This is due to the fundamental difference in how a coincidental match could have come to light. The "random match probability" that the government seeks to put before the jury answers the question, "What is the chance that an unrelated¹⁴ randomly selected person would happen to match the evidence profile? This is an appropriate question in a "confirmation" case because, for the defendant to be innocent, the government's suspect just happened to also match the evidence DNA profile. This question is irrelevant, however, when the very reason the government suspects the person is because he was

¹⁴ All DNA statistical calculations rely on the *assumption* that no relative of the defendant could be the evidence sample donor. See David J. Balding, *Errors and Misunderstandings in the Second NRC Report*, 37 *Jurimetrics J.* 469, 473 (1997) (appended).

found to match the evidence profile after authorities had trawled through thousands of persons to find it. No amount of subsequent retesting can ever convert this situation back into a “confirmation” case.

Consider for example a case where an eyewitness describes her attacker but the attack left her blind and unable to engage in an identification procedure. A suspect is nonetheless developed based upon, say, suspicious actions near the crime scene. If the victim describes her attacker very precisely, naming eight unusual visible characteristics (*e.g.*, male, 5’10” tall, 160 pounds, 30s, black, facial hair, no glasses, and dark clothing), and the suspect matches every one of them, then the probative value of this match is great. If the circumstances of making him the suspect were just unfortunate coincidences and he is innocent, one would ask, “But what are the chances a randomly selected person just happens to share the eight distinctive visible characteristics as the assailant?” This is the form of question that is relevant in a “confirmation” case.

Suppose instead that no leads were developed after the attack. Inspired by the detail in the description, the police start looking through DMV photographs. Eventually, after looking through many thousands, they come across a person who matches all eight characteristics. In this instance it would not be appropriate to ask “What are the chances a randomly selected person would just happen to share the eight distinctive visible characteristics as the assailant” because the new suspect was not randomly selected. Rather, he was selected for the very reason he shared those traits. Common sense shares the lesson of statistics that if you look through thousands of samples for something rare, you are more likely to come across it than if you look at only one. “[T]he argument is essentially the same as for a lottery; if P is the probability of winning with one ticket, the probability of winning with N tickets is NP.” Newton E. Morton, *The Forensic DNA Endgame*, 37

Jurimetrics J. 477, 499 (1997) (appended).¹⁵

Scientists unanimously acknowledge this difference between a “cold hit” case and a “confirmation” case.

[T]he more extensive was your search, the less impressed I am. The reason is that among many comparisons, it is unsurprising that one of them will, “by chance,” display results that, on their own, might be regarded as significant. In this setting, the effect of the search is to weaken evidential strength. This phenomenon is widely understood by scientists. Indeed, conveying the idea to the general public is often regarded as a major challenge in advancing the public understanding of science.

David J. Balding, *Errors and Misunderstandings in the Second NRC Report*, 37 Jurimetrics J. 469, 471 (1997) (appended).

The National Research Council of the National Academy of Sciences has twice issued “blue ribbon” reports that deal with DNA evidence, including DNA evidence derived from “cold hits.” As to the stark difference between “confirmation” and “cold hit” cases, the NRC reports agree. “The distinction between finding a match between an evidence sample and a suspect sample and finding a match between an evidence sample and one of many entries in a DNA profile database is important. The chance of finding a match in the second case is considerably higher.” National Research Council, *DNA Technology in Forensic Science* 124 (Nat’l Acad. Press 1992) (“NRC I (1992)”) (selected portions appended). “There is an important difference between [the “confirmation” case] and one in which the suspect is initially identified by searching a database to find a DNA profile matching that left at a crime scene. In the latter case, the calculation of a match probability or L[ikelihood]R[atio] should take into account the search process.” National Research Council, *The Evaluation of Forensic DNA Evidence* 134 (Nat’l Acad. Press 1996) (“NRC II

¹⁵ This example also illustrates why retesting cannot convert a “cold hit” case into a “confirmation” case. No matter how many times you ask the victim to describe the same eight traits or how many times you look at the suspect’s features, they will still be the same. Likewise, the reason the person is being suspected will always be the same – because he was searched for based on those very traits.

(1996)”) (selected portions appended). *See* NRC II (1996) at 161 (“If the suspect is identified through a DNA database search, the interpretation of the match probability and likelihood ratio . . . should be modified.”). The DNA Advisory Board, which was led by the FBI, also agrees that “cold hit” cases are qualitatively different than “confirmation” cases and, because “the probability of identifying a DNA profile by chance increases with the size of the database[,] this chance event must be taken into account when evaluating value of the matching profile found by a database search.” DNA Advisory Board, *Statistical and Population Genetics Issues Affecting the Evaluation of the Frequency of Occurrence of DNA Profiles Calculated from Pertinent Population Database(s)*, 2 *Forensic Sci. Communications* 1, 5 (July 2000) (appended).

The reason that scientists pay particular attention to “cold hits” is because, as in the blinded-witness example above, when an individual is identified through a database trawl, there is the very real danger that an innocent person, who coincidentally shares an identical profile at the evidence loci, will be caught up in the net. There have been too many examples of two persons sharing genetic profiles on low-number loci comparisons to fail to account for the unfortunate reality that database searches can lead to false matches and can generate inflated probability statistics. *See, e.g.,* Kathy Troyer *et al.*, *A Nine STR Locus Match Between Two Apparently Unrelated Individuals Using AmpF/STR Profiler Plus and Cofiler*, presented at 12th International Symposium on DNA Identification (Phoenix, Ariz. 2001) (appended) (reporting 9-location DNA profile match between two unrelated individuals (one white, one black) in state DNA database); Department of Justice, National Institute of Justice, *The Future of Forensic DNA Testing* 25 n.13 (Nov. 2000) (reporting ten 6-location DNA profile matches in New Zealand database of 10,907 records in which eight of matches were brothers and two of matches were unrelated persons); Richard Willing, *Mismatch Calls DNA Tests into Question*, *USA Today* (Feb. 8, 2000), at 3A (reporting in-

stance of false match involving 6-location DNA search in UK database) (appended); cf. Keith Moor, *Experts Dispute DNA Claims in Leskie Case*, Herald Sun (Dec. 11, 2003) (appended), available at <http://www.newstest.com.au> (10-loci match was either coincidental as opined by Australian crime lab director or result of contamination).

Notwithstanding that all experts agree that the statistics are different in “cold hit” cases, the remaining debate is about what method should be used to report those statistics. And here, there is no agreement.¹⁶

B. The Position Espoused by the Scientists in NRC I (1992) and Espoused by a Number of Scientists Today is that the Loci Used in the Database Search Should not be Part of a Random Match Probability Calculation.

The first method to deal with this problem was promulgated in 1992 by the first body of experts appointed to the Committee on DNA Science by the National Research Council.¹⁷ This panel concluded that selection bias invalidates the use of searched profiles at trial:

The distinction between finding a match between an evidence sample and a suspect sample and finding a match between an evidence sample and one of many entries in a DNA profile databank is important. The chance of finding a match in the second case is considerably higher, because one does not start with a single hypothesis to test (i.e., that the evidence was left by a particular suspect) but instead fishes through the databank, trying out many hypotheses. . . .

When a match is obtained between an evidence sample and a databank entry, the match should be confirmed by testing with additional loci. The initial match should be used as probable cause to obtain a blood sample from the suspect, but only the statistical frequency associated with the additional loci should be presented at trial (to prevent the selection bias that is inherent in searching a databank). Forensic DNA typing laboratories should recognize that they will require additional loci beyond those used in the databank to prove a case against a suspect.

¹⁶ In an attempt to help clarify the distinctions among the three separate approaches, Mr. Jenkins has obtained a sworn declaration from Dr. Sandy L. Zabell, Professor in the Departments of Mathematics and Statistics at Northwestern University. Dr. Zabell’s declaration uses examples to walk through the differing statistical approaches and is provided, along with his curriculum vitae, in the Appendix.

¹⁷ The panel of experts that generated NRC I (1992) included Drs. Mary-Claire King, Richard Lempert, Eric Lander, Ruth Macklin, Thomass Marr, Victor McKusick, and Phillip Reilly.

NRC I (1992) at 124.

The primary criticism leveled against this approach, and recognized by NRC I (1992) itself, *id.*, is that, out of concern that the database match was purely coincidental such that an innocent person might get charged with an offense, NRC I (1992) elects to not use all the information available to determine identity. Rather, some loci are used solely for the database trawl and are subsequently discarded if the analyst goes on to compare the “cold hit” person’s genetic profile to that of the crime scene evidence. So, for example, if the database search that generated the “cold hit” used 10 particular loci, those same 10 loci could not be used for the subsequent comparison between the “cold hit” suspect’s profile and the crime scene evidence profile. Rather, the forensic laboratory should use additional, different loci in making its comparison. Depending on the number and specifics of the additional loci used, this procedure could dramatically reduce the government’s random match probability calculations by a number of magnitudes.

DNA forensic laboratories have the core 13 CODIS loci -- and another 8 loci, at their disposal for forensic DNA identification. See <http://www.promega.com/techserv/apps/hmid>, <http://www.promega.com/geneticidproc/ussymp7proc/ab60.html> (together listing 21 separate loci, plus an additional loci to determine gender, that can be forensically tested).¹⁸ Hence, as discussed above, the federal CODIS program uses 13 loci to generate a convicted offender profile and Virginia now uses 14 loci to generate its convicted offender profiles. Given the abundant number of

¹⁸ The 13 CODIS loci are: CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, and D21S11. Powerplex 16 also includes Penta D & Penta E (and Amelogenin, the gender-determinative locus). Powerplex ES includes SE33. All of this information can be cited to <http://www.promega.com/techserv/apps/hmid/>. In addition, the published protocol for the Geneprint Fluorescent STR System (known as Silver STR) lists the additional loci as F13A01, FESFPS, F13B, HPRTB, LPL. The cite is: <http://www.promega.com/geneticidproc/ussymp7proc/ab60.html>.

genetic markers available at the present time, even as some scholars have criticized and proposed alternatives to this approach, *see infra* Parts II.C and II.D, NRC I (1992)'s approach currently enjoys a number of followers.

For example, Newton E. Morton, Professor, Human Genetics, University of Southampton opined a 1997 peer-reviewed article in *Jurimetrics*: “As recognized by NRC I [(1992)], the best solution is to confirm a match by a panel of marker independent of the ones used in trawling in the database. This evidence is free of ascertainment bias, and the corresponding likelihood ratio can be presented as evidence without indicating that the defendant was identified through a criminal database.” Morton, *supra*, at 489. Writing separately in that volume of *Jurimetrics*, Dr. Richard Lempert, who served on the committee that produced NRC I (1992), affirmed his belief that NRC I (1992) best presented the manner in which to report “cold hit” DNA statistics. Richard Lempert, *After the DNA Wars: Skirmishing With NRC II*, 37 *Jurimetrics J.* 439, 461-62 (1997) (appended). *See also* Aidan Sudbury, *Comment to David J. Balding & Peter Donnelly, Inference in Forensic Identification*, 158 *J. Royal Stat. Soc. A*, Par 1, 21, 48-49 (1995) (appended) (agreeing with substance of NRI I (1992)).

Furthermore, Mr. Jenkins has interviewed several other experts who are currently involved in the interpretation of forensic DNA evidence who endorse NRC I (1992)'s method. Dr. Laurence Mueller, a professor in the Ecology & Evolutionary Biology Department at the University of California-Irvine who frequently testifies about forensic DNA, opines: “This approach can both take advantage of a genetic database as an investigative tool and yield probative evidence that can be evaluated by the same statistical techniques used in standard cases. There exist today a sufficient number of genetic markers to allow the creation of a useful database and the production of probative forensic evidence.” Sworn Declaration of Dr. Laurence D. Mueller, at 3-4, para. 12 (Apr. 2, 2004)

(appended with curriculum vitae). Professor Dan Krane, a professor in the Department of Biological Sciences at Wright State University who has conducted his own analyses of population databases, believes that NRC I (1992)'s approach is the only way to "consistently generate conservative statistics that still reflect the power of DNA typing methodologies." Sworn Declaration of Dr. Dan E. Krane, at 5, para. 8 (April, 2, 2004) (appended with curriculum vitae).¹⁹

C. The Position Espoused by the Scientists in NRC II (1996), a Report that the Government Relied Heavily Upon in *Roberts/Veney*, Is that the Random Match Probability Should be Modified by Multiplying It by the Number of Persons Searched in the Database.

By 1996, as DNA databases were gaining in practice, some scientists developed a different view as how DNA evidence in "cold hit" cases should be interpreted, though they continued to recognize that "cold hit" cases were different than the typical forensic DNA case. This approach was set forth in the NRC II (1996) report. "A special circumstance arises when the suspect is identified not by an eyewitness or by circumstantial evidence but rather by a search through a large DNA database. If the only reason that the person becomes a suspect is that his DNA profile turned up in a database, *the calculations must be modified.*" NRC II (1996) at 32 (emphasis added). NRC II (1996) discussed two approaches. These scholars believe that a "cold hit" match is less probative than a single DNA match since the chance of finding a match to a particular evidence DNA profile increases as it is compared to more people. Thus, for example, finding that single person chosen at random is left-handed is somewhat unusual but finding at least one left-handed person in a sample of 1000 is not at all surprising. The committee in NRC II (1996) offered a different method to account for the risk of a coincidental match in a large database: "Multiply the match probability by the size of the database searched. This is the procedure we recommend." *Id.*

¹⁹ Should this Court conclude that the government is entitled to a hearing to determine admissibility, Mr. Jenkins proffers that he will be able to provide the names of other prominent scientists who endorse NRC I (1992)'s position.

The proponents of this method believe that the NRC I (1992) approach is too conservative. on the ground that while “a sound procedure,” “it wastes information, and if too many loci are used for identification of the suspect, not enough might be left for an adequate subsequent analysis.” *Id.* Their alternative method differs in three ways: 1) no testing is performed at additional loci; 2) genetic markers used in the original database search are included in the statistical calculations, and 3) the size of the database being searched (N) is taken into consideration.

This group of scientists believes that the larger the searched database, the less reliable is the DNA identification of a suspect identified from the database. So, for example, if the RMP is 1 in 1,000,000, and the number of profiles in the database is 100,000, the corrected RMP would be 1 in 10,000. As shown by the example, the match probability presented to the jury is reduced significantly under the NRC II (1996) approach.

This approach was immediately and virulently attacked by a third group of scholars, discussed *infra* in Part II.D., who take the polar opposite position and believe that the larger the searched database, the more reliable is the DNA identification of a suspect identified from the database. Notwithstanding those attacks, statisticians and other supporters of NRC II (1996) have stood their ground and reaffirmed the correctness of their position and the incorrectness of that of their opponents. *See, e.g.,* Anders Stockmarr, *Likelihood Ratios for Evaluating DNA Evidence When the Suspect is Found Through a Database Search*, 55 *Biometrics* 671 (Sept. 1999) (appended); Anders Stockmarr, *Reply to Comment on Stockmarr’s “Likelihood Ratios for Evaluating DNA Evidence When the Suspect is Found Through a Database Search*, 57 *Biometrics* 978 (Sept. 2001) (appended); Anders Stockmarr, *Reply to Ewett Letter to the Editor of Biometrics*, 56 *Biometrics* 1275 (Dec. 2000) (appended); Bernie Devlin, *The Evidentiary Value of a DNA Database Search*, 56 *Biometrics* 1276 (Dec. 2000) (appended).

D. A Third Set of Scholars Rejects the Classical Statistics Methodologies of the Two NRC Reports and Holds that Using a Statistical Method Known as the Likelihood Ratio Approach, Evidence of Probability is Stronger, not Weaker, When the Suspect is Identified from a Database Trawl.

The third group of scientists is comprised of individual scientists who have published peer-reviewed papers in which they argue that a “cold hit” should actually be given *more, not less*, weight than a match found in a “confirmation” case. *See, e.g.*, David J. Balding & Peter Donnelly, *Evaluating DNA Profile Evidence When the Suspect is Identified Through a Database Search*, 41 J. Forensic Sci. 603 (July 1996) (appended) (“[W]e argue that in a situation in which exactly one matching individual is found from a database search, the strength of the DNA evidence against that individual is *not* reduced relative to [a “confirmation” case]. In fact, in the database search case, under reasonable assumptions, the DNA evidence will be slightly stronger than in the probable cause setting.”). Their position is based on the thinking that not only has the defendant been found to match the evidence, but also many more individuals have been found not to match. *Id.* at 605. To these scientists, in “confirmation” cases where only a single match is found during the course of DNA testing, there is at least still a formal possibility that one or more untested people may also match the evidence, and that possibility becomes increasingly less likely as the database used for a cold hit becomes larger.

For a selection of relevant publications, each appended, see David J. Balding, *The DNA Database Search Controversy*, 58 Biometrics 241 (March 2002); David J. Balding, *Errors and Misunderstandings in the Second NRC Report, supra*; David J. Balding & Peter Donnelly, *Inference in Forensic Identification*, 158 J. Royal Statistical Socy., Series A (21 (1995); A.P. Dawid, *Comment on Stockmarr’s “Likelihood Ratios for Evaluating DNA Evidence When the Suspect is Found Through a Database Search*, 57 Biometrics 976 (2001); A.P. Dawid & J Mortera, *Coherent Analysis of Forensic Identification Evidence*, 58 J. Royal Statistical Socy., Series B, 425 (1996); Ian

W. Evett et al., *Letter to the Editor of Biometrics*, 65 *Biometrics* 1274 (Dec. 2000); Ian W. Evett & Bruce S. Weir, *Interpreting DNA Evidence: Statistical Genetics for Forensic Scientists* 219-22 (Sinauer Assocs. 1998); and Michael O. Finkelstein & Bruce Levin, *On the Probative Value of Evidence from a Screening Search*, 43 *Jurimetrics J.* 265 (Spring 2003).

These scientists reject the “classical statistics” orientation of NRC I (1992) and NRC II (1996):

[Classical statisticians] grew up to facilitate objective inferences from data. Classical statisticians try to avoid subjective judgments, seeking instead to determine what conclusion can be drawn solely on the basis of frequency of observation. [Our] Bayesian approach – updating the odds assigned to a given proposition in light of evidence subsequently received – is thus unacceptable to classical statisticians because it depends on the subjective assignment of odds in the absence of objectively measurable data. . . .

...

It is considered bad science to trawl data, looking for surprising results and then proclaiming that the data proves a proposition that would likely lead to such results. . . .

Peter Donnelly & Richard D. Friedman, *DNA Database Searches and the Legal Consumption of Scientific Evidence*, 97 *Mich. L. Rev.* 931, 966-68 (Feb. 1999) (appended). These scientists reject the random match probability calculation, whether corrected or not. Instead, they rely solely upon the determination of a likelihood ratio. Their form of statistical analysis, known as “Bayesian,” requires making statistical assumptions as to the prior odds for an individual. They present a powerful statistical argument that has yet to gain currency in United States courts.

Their method differs from NRC I (1992)’s approach in three ways: 1) no testing is performed at additional loci; 2) genetic markers used in the original database search are included in the statistical calculations; and 3) the size of the database being searched (N) is taken into consideration. Their method also differs from the NRC II (1996)’s approach in one, extremely fundamental way. To this group of experts, the effect of the database size on the significance of a

match is precisely the opposite – large databases generate the most damning statistics for a defendant while, in the NRC II (1996) approach, the larger the database the less damning the statistics become to a defendant. Thus, the second and third approaches are diametrically opposed – in scientific theory and in practical consequences -- with respect for implications of the size of the database that is searched.

E. There is Bitter, Irreconcilable Conflict and Controversy Among the Three Groups.

The disagreement among the relevant experts is open and unresolved. The most recent article on the subject is even titled, “The DNA Database Search Controversy,” Balding, *The DNA Database Search Controversy, supra*. That article opens, “[M]any of the statistical issues are now largely resolved. One of the areas where consensus remains incomplete concerns the effect of database searches on evidential strength.” *Id.* at 241. *See also id.* at 243, 244 (further reporting on “controversy” among statisticians). Thus, as demonstrated above, in 2000, *Biometrics* published a bitter back-and-forth, provided in the Appendix, between Drs. Sensabaugh and Devlin’s supporting NRC II (1996) on the one hand and Drs. Evett, Foreman, and Weir, quoting Drs. Balding and Donnelly’s counterapproach, on the other. Similarly, in 1997, *Jurimetrics* published a collection of articles disagreeing with one another on the proper meaning of this evidence, and those articles too are included in the Appendix.

And the experts are not mincing words in their disagreement. Dr. Balding refers his readers to Dr. Stockmarr’s 1999 *Biometrics* article to observe the “flaws” in NRC II (1996)’s reasoning and calls Dr. Devlin’s support of NRC II (1996) “flawed” with reasoning that has “no bearing on the issues” and with an approach that “makes little sense.” Balding, *The DNA Database Search Controversy, supra*, at 243.

Even the FBI recognizes the dispute noting that, with neither camp’s view clearly superior –

or – inferior to that of the other, “we are left with an interesting dilemma.” DAB, *Statistical and Population Genetics Issues*, *supra*, at 7. In discussing the battle between the NRC II (1996) camp and the Balding/Donnelly camp, the DNA Advisory Board wrote: “Both camps appear to present rigorous arguments to support their positions. Indeed, the proper treatment superficially appears to rest in the details of arcane mathematics. . . . Curiously, the mathematics underlying both approaches is correct, despite the apparently divergent answers. It is the foundations of the formulations that differ, and they differ substantially.” *Id.* at 6-7.

In the end, of course, the question for this Court is not which of the three divergent positions is the correct one. *Porter II*, 618 A.2d at 634. The question is whether the government is able to prove that there is general acceptance as to any one of them. *Id.* There clearly is not, and the government should therefore be excluded from admission of the DNA evidence in Mr. Jenkins’ trial.

F. The Failure to Take into Account the Mathematical Possibility That a False Positive Contributed to the “Cold Hit” of Mr. Jenkins’ Profile in the Virginia Database Requires Exclusion of the DNA Evidence.

In “cold hit” cases in which the DNA match itself makes the defendant a suspect, often, like here, there is little other evidence against the defendant. The absence of other evidence makes the DNA evidence, and the proper statistical presentation of that evidence, all the more important. Scientists across the board acknowledge the possibility of handling or laboratory error leading to a false positive match, *see, e.g.*, Balding, *Errors and Misunderstandings in the Second NRC Report*, *supra*, at 475.²⁰ “Anything is possible, counsel,” as some witnesses like to say. That possibility

²⁰ A number of commentators have long expressed that consideration of error rates is crucial to an accurate determination of the probability that the report of a match signals that the defendant is actually the source of the DNA:

Although a precise probability cannot be associated with the chance of laboratory

must be mathematically measured to maximize accuracy and ensure fairness in the presentation of the DNA evidence.

The question of how the probability of a false positive affects the value of DNA evidence was raised in an article by that name in the *Journal of Forensic Science* last year. See William C. Thompson, *et al.*, *How the Probability of a False Positive Affects the Value of DNA Evidence*, 48 *J. Forensic Sci.* 1 (Jan. 2003) (appended). There, the authors noted that

[t]he potential for false positives may be a particularly important consideration when evaluating DNA evidence in trawl cases where the prior probability that any particular suspect is the source of an evidentiary sample is very low. In such cases, a key issue is whether the DNA match is sufficiently probative to create a high posterior probability that the suspect is the source despite the low prior probability. The results reported in Table 1 suggest that the probability of a false positive may be a critical factor in determining whether the DNA evidence is indeed strong enough.

Id. at 6. The authors then go on to use an example to show how circumstances under which even low false positive probabilities are of concern.

Consider, for example, the hypothetical cases reported in Table 1 in which the prior odds that the suspect is the source of an evidentiary sample are 1 in a thousand and the random match probability is 1 in a billion. If the probability of a false positive is zero, then the posterior odds are a million to one in favor of the suspect being the source, which certainly seems high enough to justify confidence in that conclusion. In other words, the DNA evidence has more than enough probative value to make up for the low prior probability. However, if the false positive probability is even 1 in 10,000, the posterior odds in favor of the suspect being the source are reduced drastically to only 10:1. *It is very important for those evaluating DNA*

error, error rates in other types of forensic laboratory tests and the results in the few blind proficiency tests done to date suggest that false positive error rates in DNA tests must be many orders of magnitude higher than the random DNA match probabilities often given juries.

Lempert, *After the DNA Wars: Skirmishing with NRC II*, *supra*, at 446-47. See also Jonathan J. Koehler, *On Conveying the Probative Value of DNA Evidence: Frequencies, Likelihood Ratios, and Error Rates*, 67 *U. Colo. L. Rev.* 859, 869 (1996) (appended); William C. Thompson, *Accepting Lower Standards: The National Research Council's Second Report on Forensic DNA Evidence*, 37 *Jurimetrics J.* 405, 419-21 (1997) (appended) (noting need for error rate estimation to limit random match probability before it reaches jury).

evidence to understand that a false positive probability on the order of 1 in 10,000, which may seem low enough to be “safe,” may nevertheless undermine that, when combined with a low prior probability, there is still room for doubt about whether the suspect is the source of the matching sample.

Id. (emphasis added).

It is of course difficult to determine the false positive rate, though 1 in 10,000 does not seem grossly off, and, barring the ability to develop the database cold hit error rate factually (say, by determining the quality of the lab work and the clarity of the results of the VDFS and the private laboratories like Bode with which it contracts), that seems an appropriate estimation.

III. THIS COURT SHOULD EXCLUDE THE DNA EVIDENCE BECAUSE ITS PROBATIVE VALUE IS SUBSTANTIALLY OUTWEIGHED BY ITS PREJUDICIAL EFFECT.

Even should this Court conclude that the government has met its burden of admissibility under the *Frye/Dyas* inquiry, Mr. Jenkins submits that the DNA evidence should nonetheless be excluded because its probative value is substantially outweighed by the potential for prejudice. *Johnson v. United States*, 683 A.2d 1087, 1100 (D.C. 1996) (en banc).

As explained in Section II.C, the government’s random match probability calculation – inaccurately expressed as “to a reasonable degree of scientific certainty” – has minimal probative value. As NRC I committee member Dr. Richard Lempert explains, the RMP’s probative value is always limited by a larger error rate and failure to include such an error leads to jury confusion:

A scientist who testifies that false positive error never happens does not address the question the jury needs answered – namely, how likely is it that a match would be reported if the evidence DNA was not the suspect’s. Moreover, she risks misleading or confusing the jury because she uses language in a specialized way that invites misinterpretation.

Lempert, *After the DNA Wars*, supra, at 442. Dr. Lempert explains the limited probative value of the RMP alone:

Although a precise probability cannot be associated with the chance of laboratory error, error rates in other types of forensic laboratory tests and the results in the few blind proficiency tests done to date suggest that false positive error rates in DNA tests must be many orders of magnitude higher than the random DNA match probabilities often given juries. If so, the probative value of a DNA match is always limited by the chance of false positive error.

Id. at 447. Presenting the jury with two numbers, both the RMP and the laboratory's estimated false positive rate, does not solve the prejudice problem, because jurors "may tend to see the probative value of the evidence as somewhere between the two probabilities rather than treating the chance of a false positive report as limiting the probative value of the reported match." *Id.*

On the other hand, the power of the DNA evidence to mislead and confuse the jury is great. It is no surprise that jurors, most of whom do not have a background in mathematics, often "have poor intuitions when it comes to reasoning with statistics in general and forensic science statistics in particular." Jonathan J. Koehler, *The Psychology of Numbers in the Courtroom: How to Make DNA-Match Statistics Seem Impressive or Insufficient*, 74 S. Cal. L. Rev. 1275, 1279 (2001) (appended). In empirical studies, jurors tend to determine the probative value of DNA evidence based solely on the probability of a "match by chance," whether or not other factors minimize the diagnostic value of the RMP in a given case. *Id.* at 1280. This is a case in point of the so-called "exemplar cue theory," well known in psychological literature, holding that people will view the probability of an event as inversely proportional to the ease with which alternative examples are cued in their mind. *Id.* Studies have shown that if the target of a DNA match is a particular suspect, examples of coincidental matches are less likely to be "cued" in the juror's mind, and "jurors will be more likely to treat small DNA matches as conclusive proof of identity." *Id.* at 1282. In several experiments from 1998 involving mock jurors, jurors were several times more likely to convict when given an RMP as compared to the phrase "the probability that the suspect would match the blood sample if he were not their source is [X]." *Id.* at 1288.

In their analysis of the risk of errors to “cold hit” identification, Professor Thompson and his colleagues noted that jurors’ ability to understand the potential for false positives does not translate into an ability to assess the statistical significance of error:

Even if jurors understand the various ways in which a false positive might occur, it requires a leap of faith to conclude that they will therefore be able to determine accurately, based on common sense, whether, for example, the probability of such an error in a particular case is 1 in 100 or 1 in 10,000. . . . To rely on jurors’ common sense to produce accurate estimates when experts cannot agree seems unduly optimistic.

Thompson et al., supra, at 2-3. *See also* Jonathan J. Koehler, *On Conveying the Probative Value of DNA Evidence: Frequencies, Likelihood Ratios, and Error Rates*, 67 U. Colo. L. Rev. 859 (1996) (appended); Jonathan J. Koehler, *The Random Match Probability in DNA Evidence: Irrelevant and Prejudicial?* 35 *Jurimetrics J.* 201, 212 (1995) (appended). Accordingly, this Court should exclude the DNA evidence because the prejudicial effect of the evidence substantially outweighs its probative value.

IV. THE “COLD HIT” DNA EVIDENCE IN THIS CASE MUST BE EXCLUDED BECAUSE THE GOVERNMENT CANNOT ESTABLISH A PROPER CHAIN OF CUSTODY SUFFICIENT TO AUTHENTICATE THAT THE SAMPLE REPORTEDLY TO BE RAYMOND JENKINS’ IN THE VIRGINIA CONVICTED OFFENDER DATABASE WAS IN FACT HIS AND WAS PROPERLY ACCOUNTED FOR FROM THE TIME OF HIS BLOOD’S SEIZURE, THROUGH THE ANALYSIS OF HIS BLOOD FOR A PROFILE, TO THE INCLUSION OF THAT PROFILE IN THE DATABASE.

This jurisdiction has adopted Federal Rule of Evidence 901, requiring that evidence be properly authenticated, meaning reliably identified as being what it purports to be, before being admitted. Specifically, a missing link in the chain of custody that calls into question the identity of the evidence is a bar to admission. *See, e.g., Turney v. United States*, 626 A.2d 872, 873 (D.C. 1993); *Novak v. District of Columbia*, 160 F.2d 588, 589 (D.C. Cir. 1947) (urinalysis records improperly admitted where there was “missing a necessary link in the chain of identification” to

show specimen tested was defendant's urine); *cf.* D.C. Code § 16-2343.01(a)(2) (requiring proof of chain of custody to admit paternity testing results using Human Leukocyte Antigen (HLA) test)).

Specifically with respect to DNA evidence, several courts have held that gaps in the chain of custody or evidence of contamination in a sample are reasons to exclude such evidence. *See, e.g., Smith v. Deppish*, 807 P.2d 144, 159 (Kan. 1991) (DNA test results may be inadmissible based on relevance, prejudice, chain of custody, or contamination issues). In addition, the Tennessee Supreme Court found the government's proffered DNA evidence to be inadmissible due to the government's failure to prove chain of custody with respect to the hair samples:

We agree with the appellant that the trial court erred in finding that the hair samples were properly authenticated. The hairs were not identified by a witness with knowledge that the mounted hair samples were the same hairs as the ones originally taken from the victim. Further, we can find no evidence whatsoever to show how the hairs came to be mounted on the slides. We also can find no evidence to show who mounted the hairs on the slides or whether the hairs were mounted in a manner sufficiently free of contamination or alteration. Although the hairs were apparently mounted . . . by someone at the FBI, no one was able to establish this important "link" in the chain of custody.

State v. Scott, 33 S.W.3d 746, 760-61 (Tenn. 2000). Here, this Court knows absolutely nothing about the chain of custody as to Mr. Jenkins' alleged DNA sample that was included in the Virginia database. At a pretrial hearing, the government must show each link in the chain to establish a sufficient chain of custody for this Court to admit the DNA evidence from the cold hit in this case. Moreover, establishing a chain of custody is especially crucial in admitting scientific evidence that, like DNA, is "hypersensitive to contamination." *Id.* at 761 n.13. Without such a showing, the DNA evidence is inadmissible under Rule 901.

Conclusion

The concern of the *Frye* test is that courts not supplant scientists in determining the validity of scientific methods; a technique must be sufficiently tested and stable before it is introduced in a

courtroom and used to take away a citizen's physical liberty. Additionally, under *Dyas*, the cold hit DNA evidence must be sufficiently reliable to reasonably form the basis for the government's DNA expert's testimony. "Cold hit" DNA evidence is not now at the point of general acceptance in the scientific community, the government's interpretation of the test results are not sufficiently reliable, and the evidence would severely prejudice Mr. Jenkins. For the foregoing reasons, and for such other reasons that may appear to this Court at a hearing on this Motion, Mr. Jenkins respectfully requests that this Court exclude all DNA evidence from this case.

Respectfully submitted,

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CERTIFICATE OF SERVICE

I hereby certify that a copy of the foregoing Motion and accompanying Memorandum of Points and Authorities has been served, by fax, without appendix (307-2022), by hand, with Appendix, upon AUSAs Emory Cole and Michael Ambrosino, United States Attorney's Office for the District of Columbia, Felony Division, 555 4th Street, N.W., Washington, D.C. 20530, on this 5th day of April, 2004.

EDWARD J. UNGVARSKY